

005020 " 560560

WO 99/18197

09/509595

PCT/EP98/06294

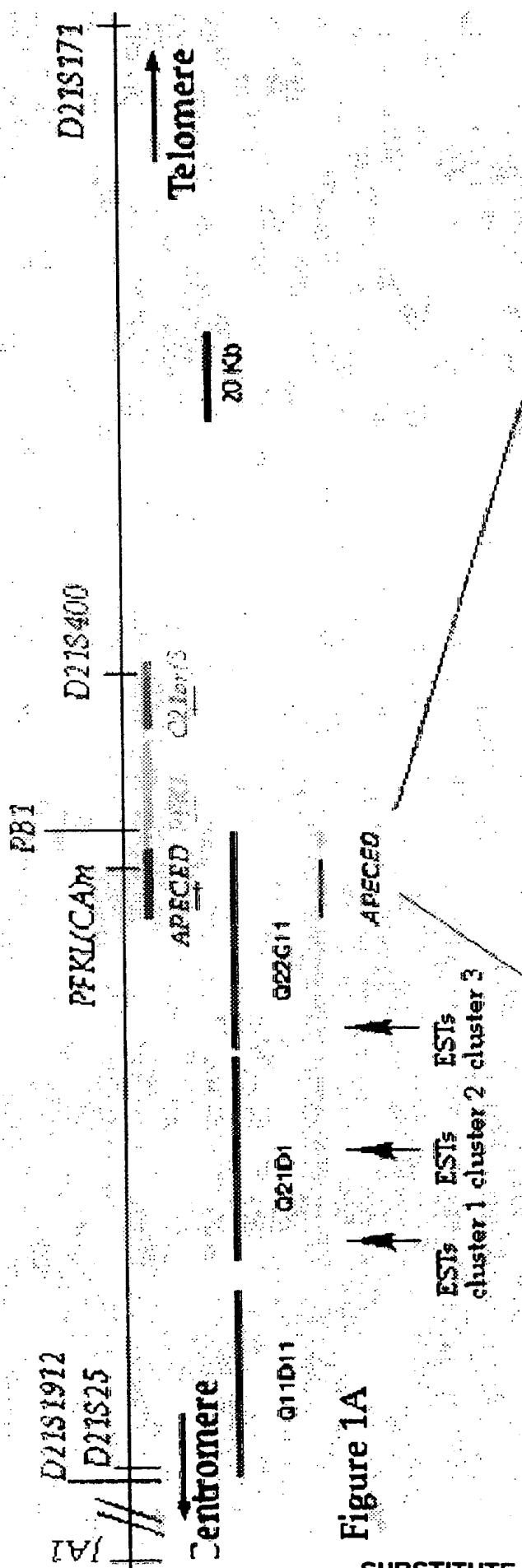
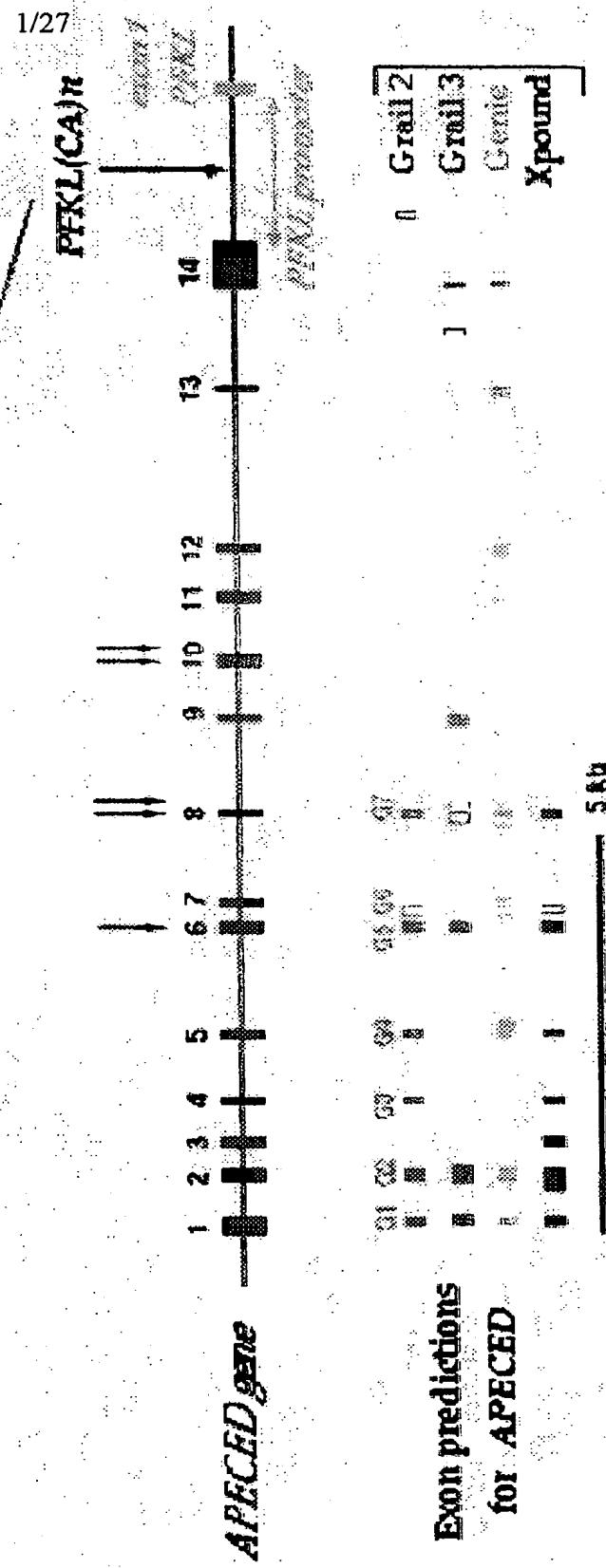


Figure 1A



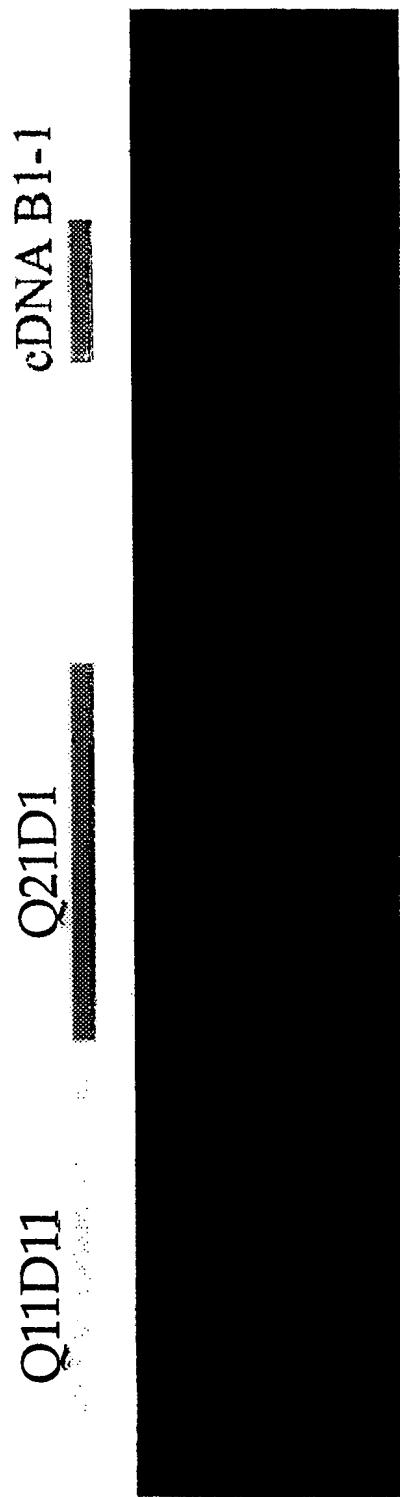


Figure 1C

3/27

1 cggccacagccggccggaggccccacagccccggggacccggaggccaaaggcagg 60  
 61 gctgccagtgtccggggacccacccgggtccggcccccagccccgggtccggccacccc 120  
 121 atggcgacggacggcgctacggccggcttctgaggctgcaacggcaggatcggggtg 180  
 1 M A T D A A L R R L R L H R T E I A V 20  
 181 gccgtggacacgcgttcccaactgtgcacgcgtggctgaccacgacgtgtcccgag 240  
 21 A V D S A F P L L H A L A D H D V V P E 40  
 241 gacaaggttcaggagacgttcatctgaaggaaaaggagggtgtccccaggccctccac 300  
 41 D K F Q E T L H L K E K E G C P Q A F H 60  
 301 gccctcctgtcctggctgtgaccaggactccacagccatccctggacttctggagggtg 360  
 61 A L L S W L L T Q D S T A I L D F W R V 80  
 361 ctgttcaaggactacaacctgtggaggcgtatggccggctgtgcaggccatccatgtggacagcttc 420  
 81 L F K D Y N L E R Y G R L Q P I L D S F 100  
 421 cccaaagatgtggacactcagcccgaggaaaggggaggaaaggccggccgtcccaag 480  
 101 P K D V D L S Q P R K G R K P P A V P K 120  
 481 gctttggtaccggccaccccgactcccaaccaaggaaaggccctcagaagaggctcgagct 540  
 121 A L V P P R L P T K R K A S E E A R A 140  
 541 gccggcccgccgtactccaaaggggcaccggcccgcccaactgtaaaggcc 600  
 141 A A P A L T P R G T A S P G S Q L K A 160  
 601 aagcccccaagaaggccggaggcaggcaggcaggcaggacgtgtggccatgtcctccactcgggaacggg 660  
 161 K P P K P E S S A E Q Q R L P L G N G 180  
 661 attcagaccatgtcagttcagttcaggagactgtggccatgtcctccggggacgtcccg 720  
 181 I Q T M S A S V Q R A V A M S S G D V P 200

FIGURE 2A

09/509595

PCT/EP98/06294

WO 99/18197

4/27

721	ggggccccggggccgtggggatccatccaggagggtttcagggttttaggttcaggcggtcc	780
201	G A R G A V E G I L I Q Q V F E S G G S	220
781	aagaagtgcattccagggtggggagttcacactccaggcaagttcgaagactccggc	840
221	K K C I Q V G G E F Y P S K F E D S G	240
841	agtggaaagaacaaggccgcaggcaggcgtggccgaaggccctctggttcagccaaaggga	900
241	S G K N K A R S S G P K P L V R A K G	260
901	gccccaggggcgctgcccccggtggagggttaggctggggccaggcaggccagggtttccc	960
261	A Q G A P G G E A R L G Q Q G S V P	280
961	gccccctctggccctccaggatcccccaagtcaccagaagaatgaggacgatgtgtgcc	1020
281	A P L A L P S D P Q L H Q K N E D E C A	300
1021	gtgtgtcggggacggggggggaggctcatctgtggacggctggccctcgggccctccacacctg	1080
301	V C R D G E L I C C D G C P R A F H L	320
1081	gcctgcctgtccctccgctccggaggatccccaggatggggacactggggatgtgggtgc	1140
321	A C L S P P L R E I P S G T W R C S S C	340
1141	ctgcaggcaacagtccaggagggtgcaggccccggcaggaggccccccaggagccca	1200
341	L Q A T V Q E P R A E E P R P Q E P	360
1201	cccggtggagaccccgctccccggggcttaggtcggggaggaggtaaagggtccca	1260
361	P V E T P L P P G L R S A G E E V R G P	380
1261	cctggggaaacccttagccggcatggacacgactttgtctacaaggccctgtccggctccg	1320
381	P G E P L A G M D T T L V Y K H L P A P	400
1321	ccttctgcaggccccgtggccaggactcctcgccctgtggactcccccctactgtgtgtg	1380
401	P S A A P L P G L D S S A L H P L L C V	420

FIGURE 2A (cont.')

1381	ggccctgagggtcaggcagaacctggctccgtgcgtttgggggtgtggagatgg	1440
421	G P E G Q Q N L A P G A R C G V C G D G	440
1441	acggacgtgtcggtgtactactgcgcgcgtgcctccactggcgctgcacttccca	1500
441	T D V L R C T H C A A F H W R C H F P	460
1501	ggcgcacctccggccgggacggggctgctgcagatcctgtcgaggagacgtgacc	1560
461	A G T S R P G T G L R C R S C S G D V T	480
1561	ccagccctgtggagggggtgctggcccccaggccccggccctggccctgcc	1620
481	P A P V E G V L A P S P A R L A P G P A	500
1621	aaggatgacactgcccgtcacggggccgtctgcacaggatgaccctggagtcctctg	1680
501	K D D T A S H E P A L H R D D L E S L L	520
1681	agcaggcacacccatcgatggcatcctgcagtggccatccagagcatggccgtccggcg	1740
521	S E H T F D G I L Q W A I Q S M A R P A	540
1741	gccccctccctccatggccggacatcgagctcgatgagagatgtgc	1800
541	A P F P S	546
1801	agaaggacacccctccctcgtcgtggaaaggccggcgtggatcaagaaggacag	1860
	<sup>Bl-1</sup>	
1861	cgccacccatgttcgtcgtggaaacacagctctgtttctggggacaccaggcat	1920
1921	catgtgcctggaaattaaaccctggccacttctactctggaaagtcccccggagcctc	1980
1981	tcctgcctggatgttcactaaaaataaaaaatgtcggtgtgggtgcgt	2040
2041	taatcccagctacatggaggcctgaggcatgagaatcactggagggtggagg	2100
2101	tgcagtgagctgagatgtggccactgcactccaggctggcaaggatgagactcgt	2160
2161	ctcaaaaaaaaacaaaaaa <sup>Bl-1</sup> accacataacataaaatttatcatcgaccatttcagt	2220
2221	tcaggccattcacatctcatgtaa	2245

FIGURE 2A (cont.)

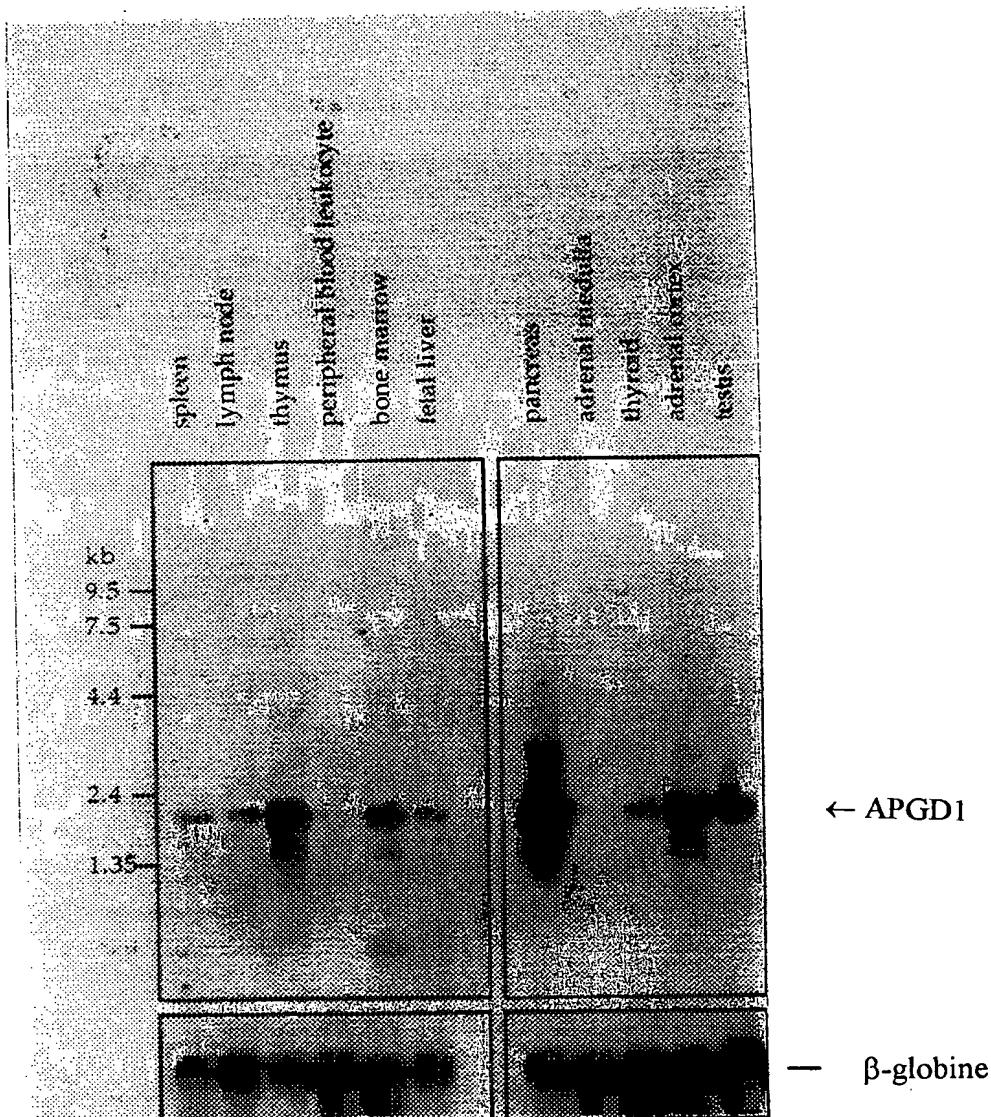
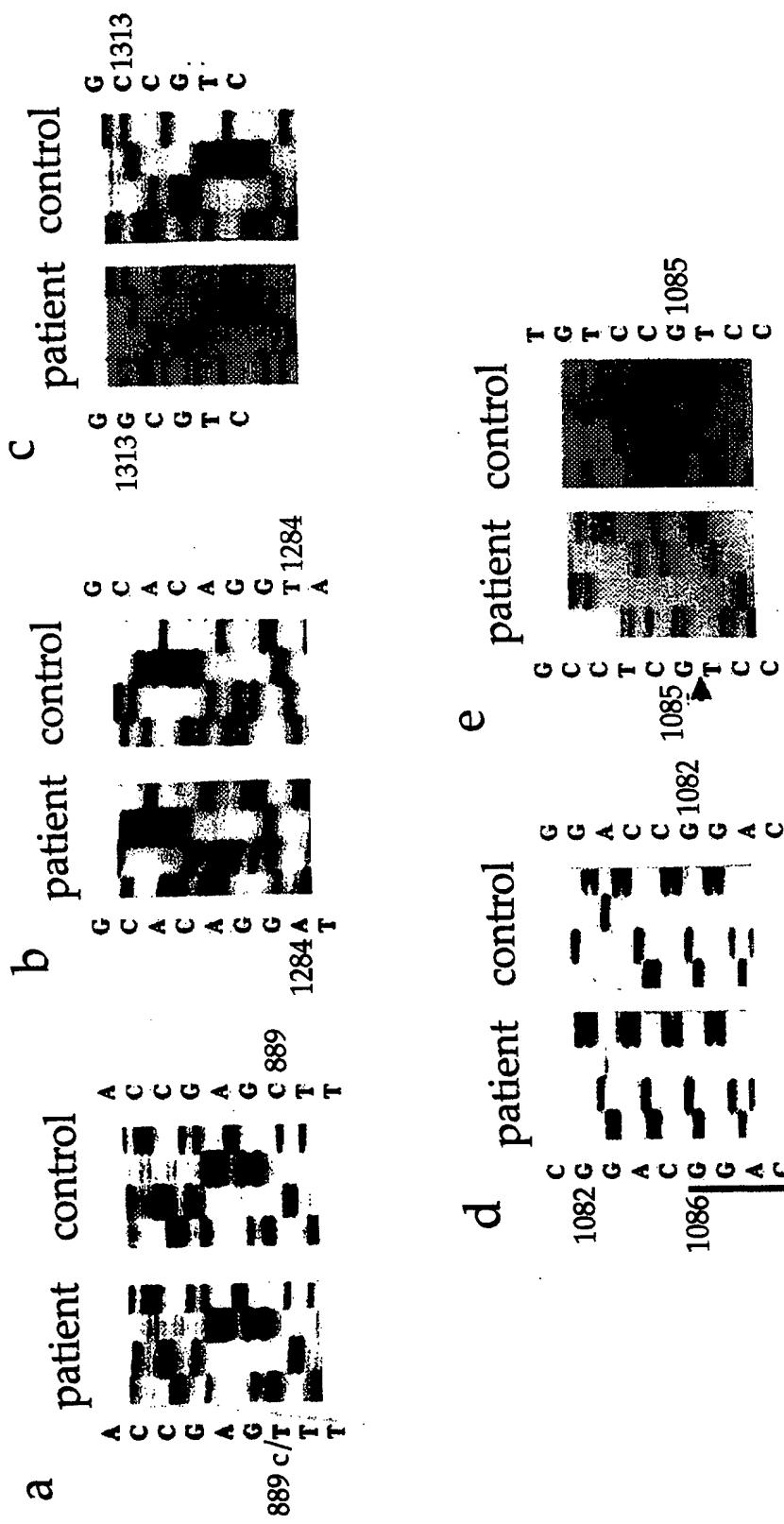


Figure 2B



The sequence lanes appear from left to right, as C, A, T, and G

Figure 3

09/509595

PCT/EP98/06294

WO 99/18197

8/27

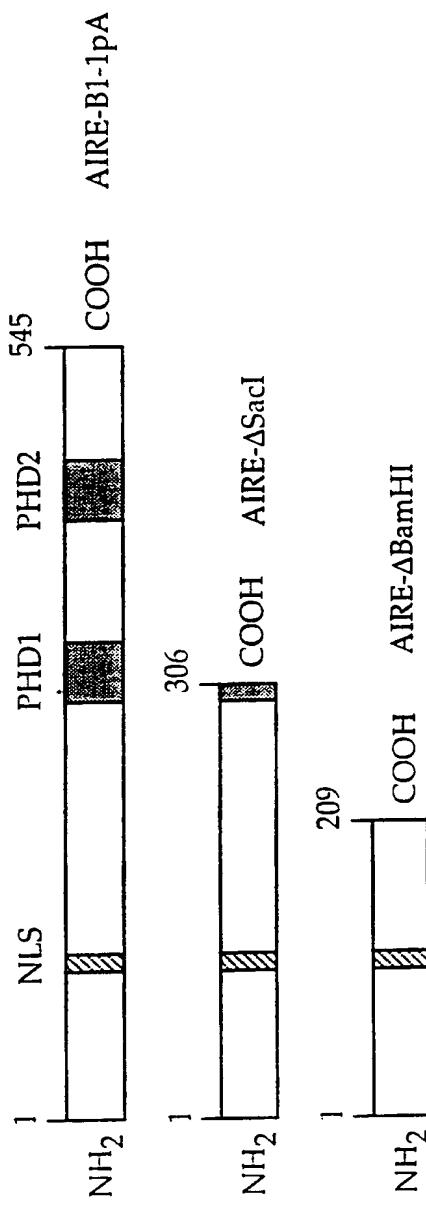


Figure 4

9/27

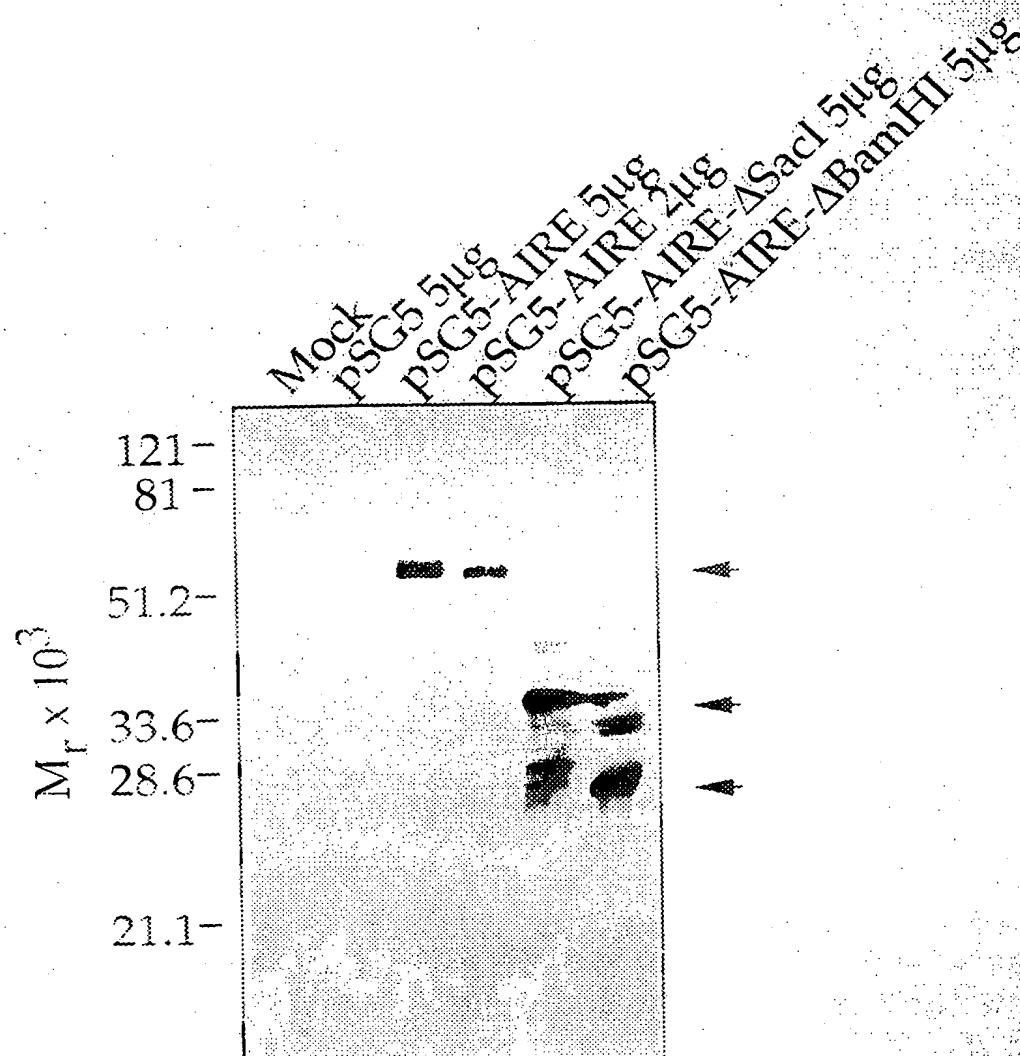


Figure 5

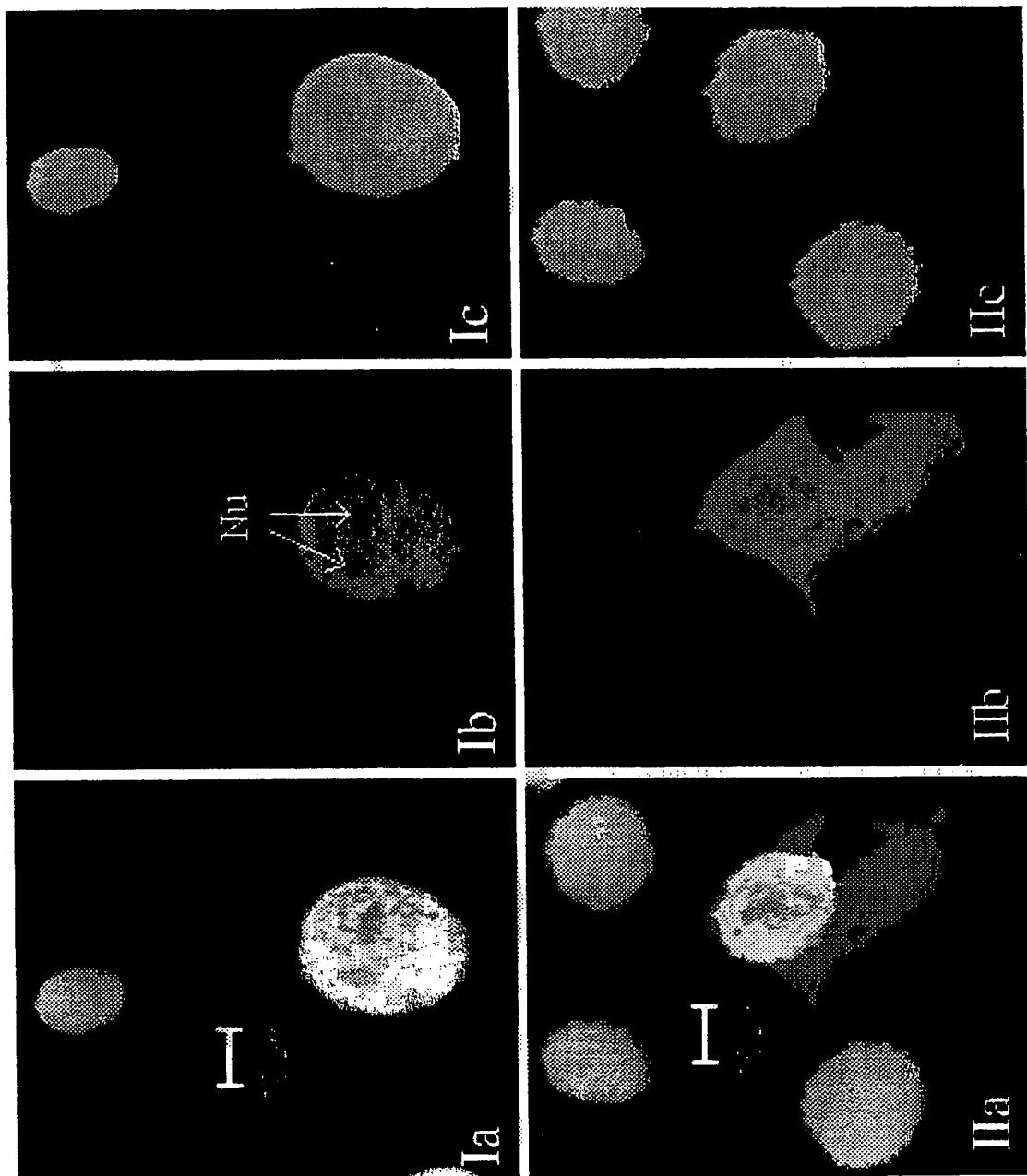


Figure 6

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11/27

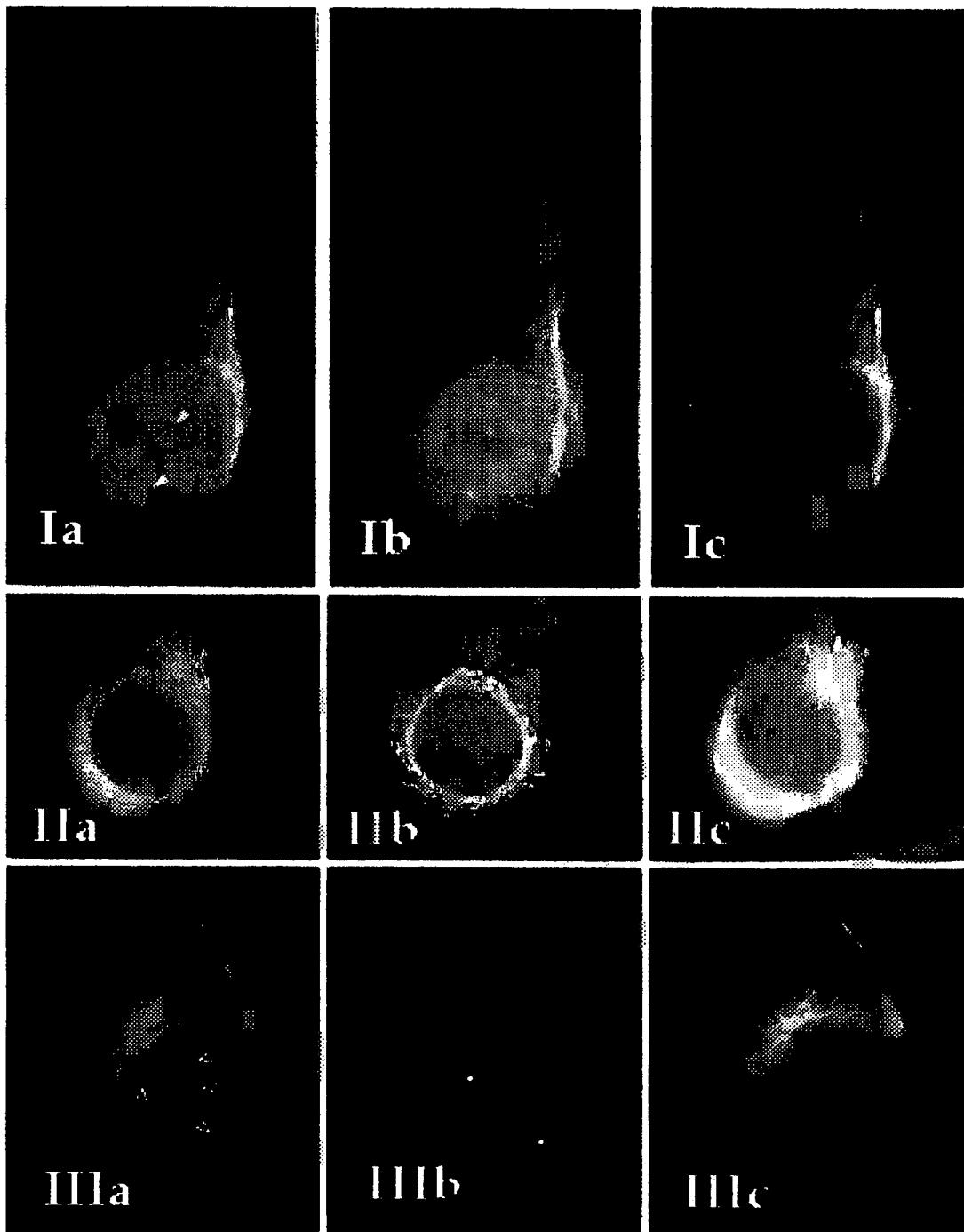
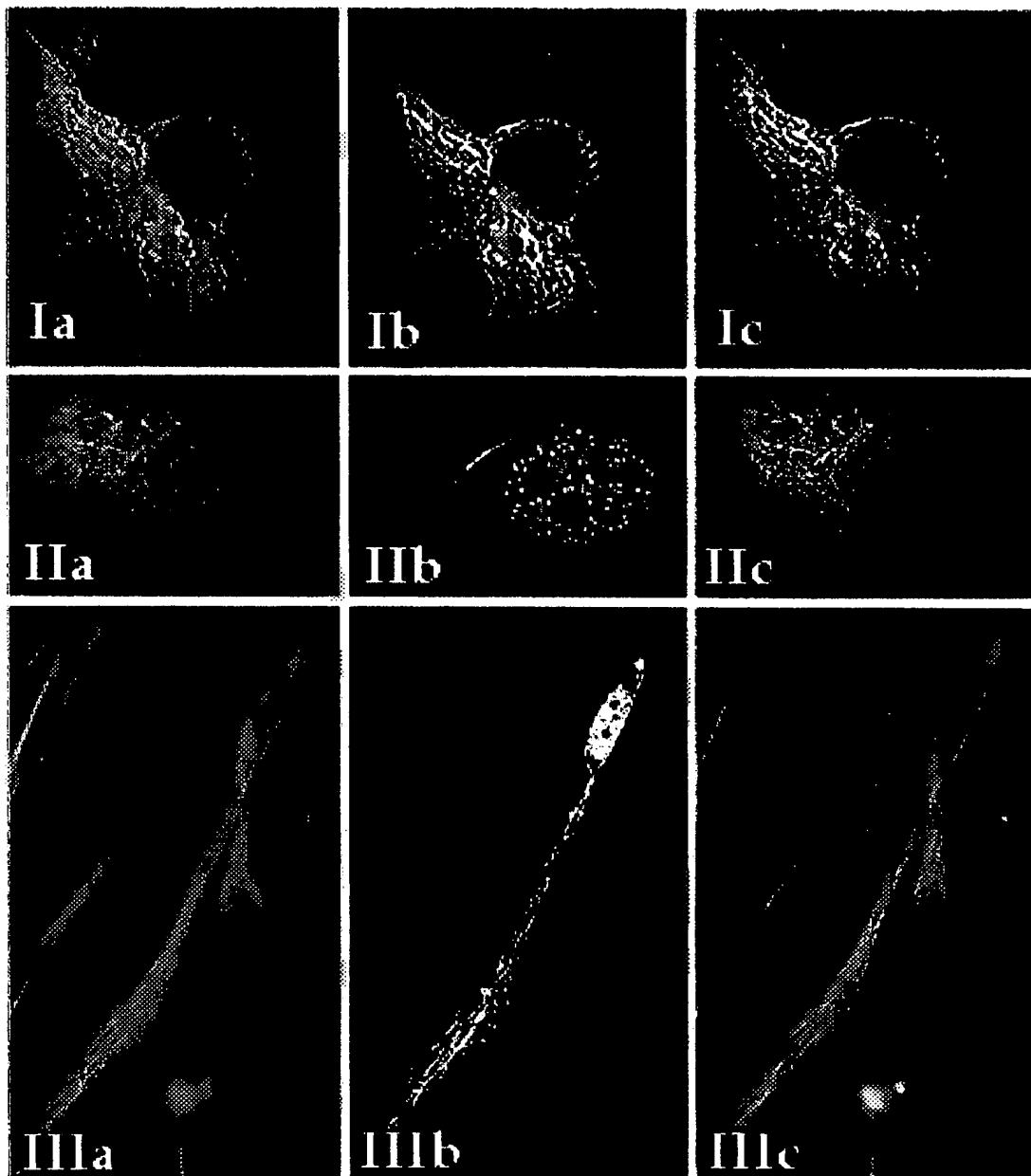


Figure 7



**Figure 8**

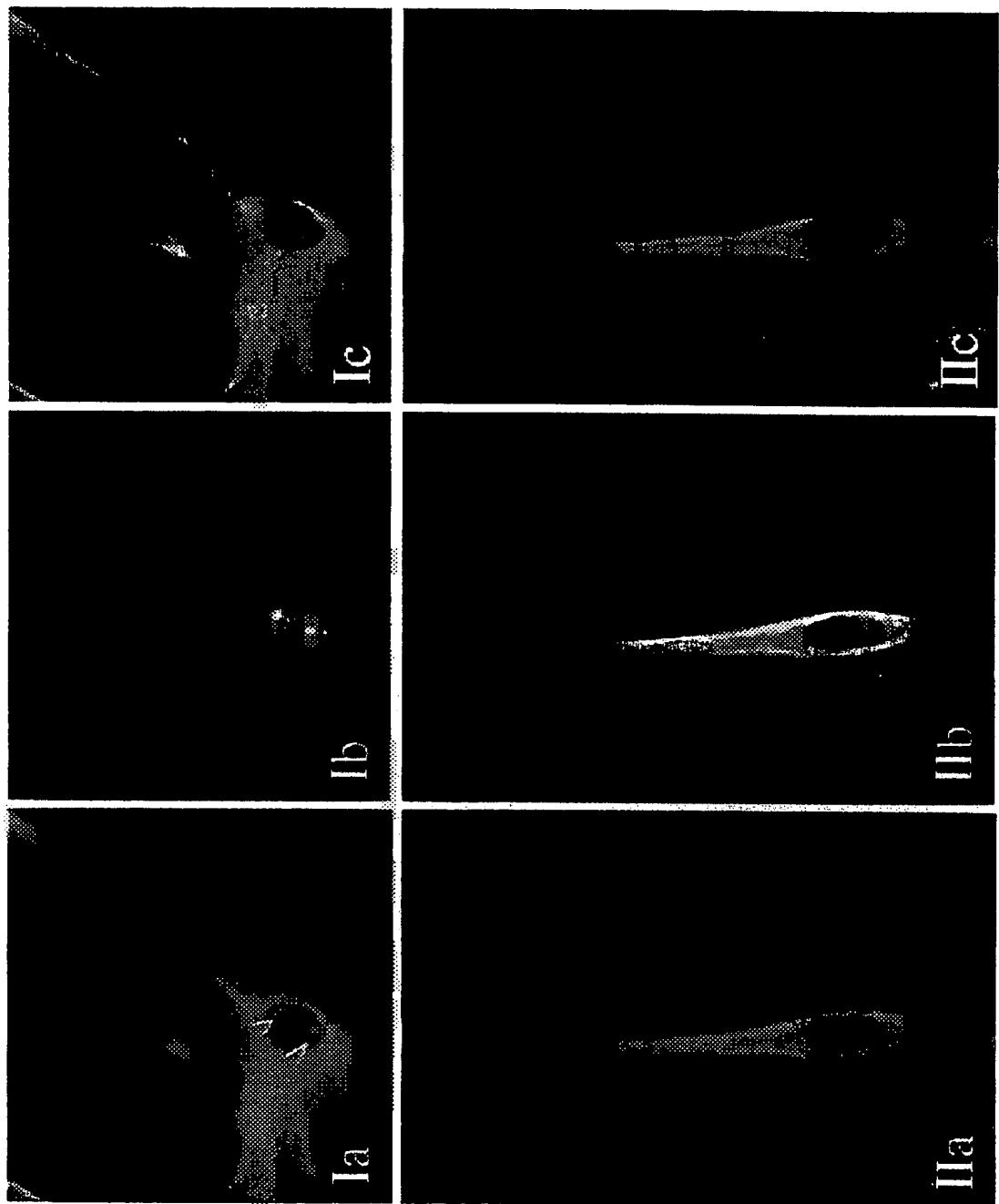
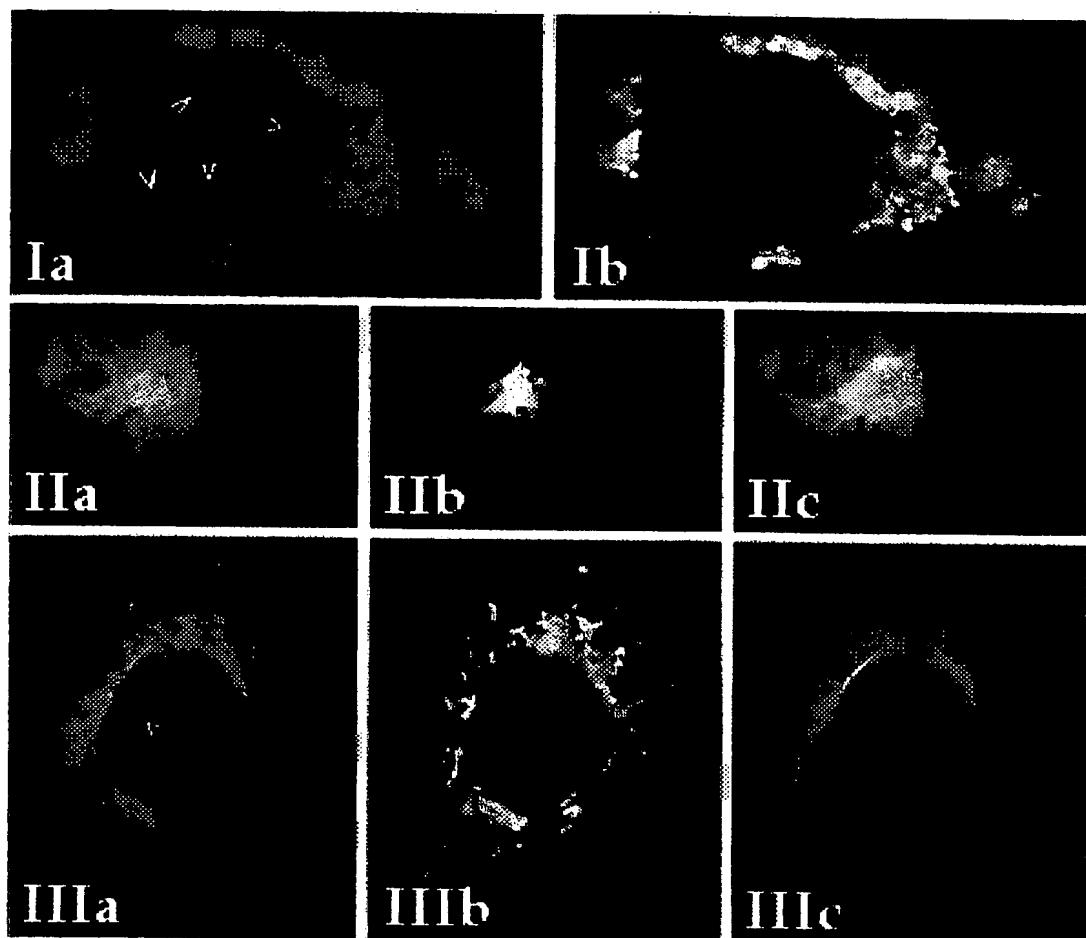
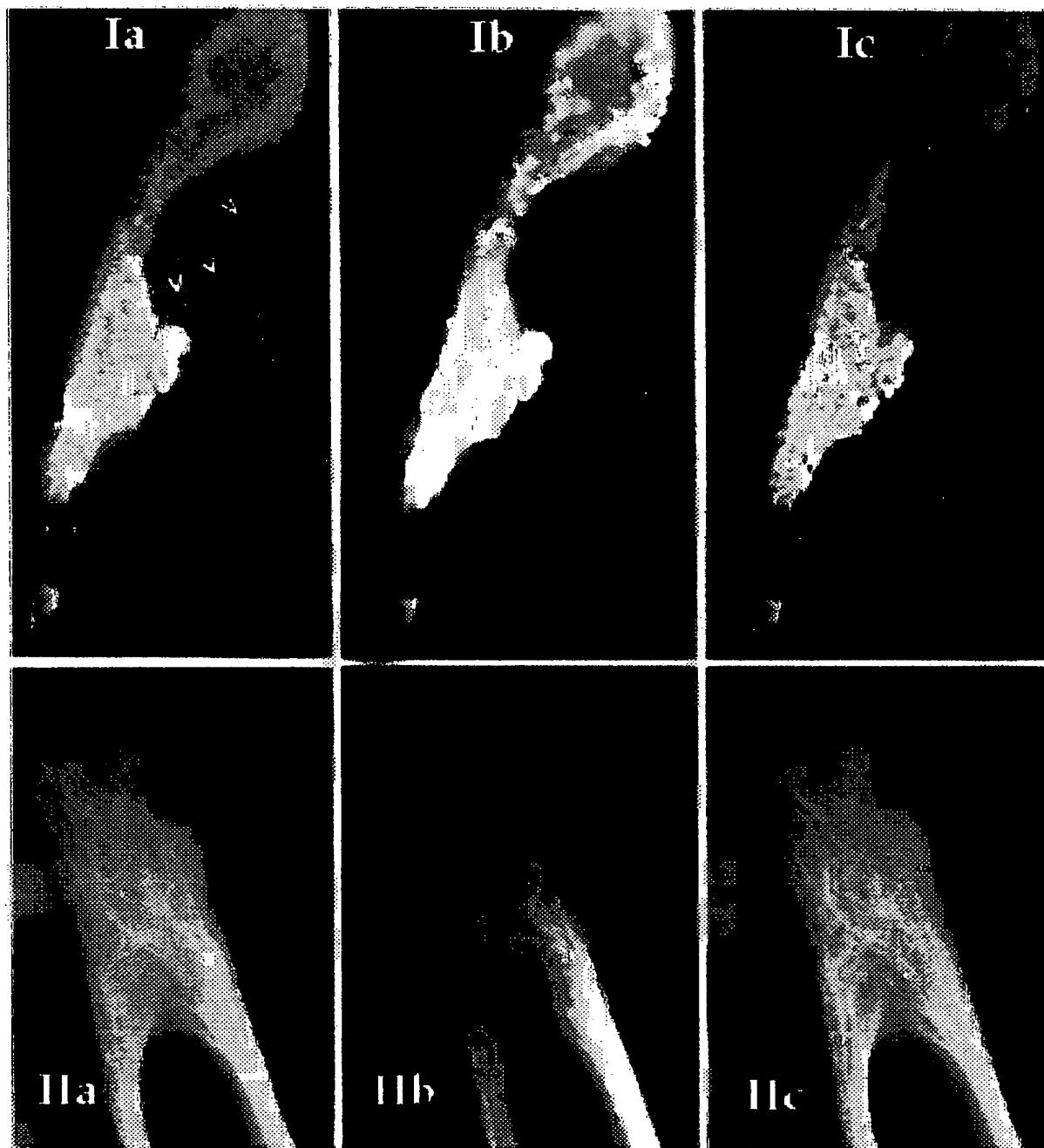


Figure 9



**Figure 10**

09509595 - 09509595



**Figure 11**

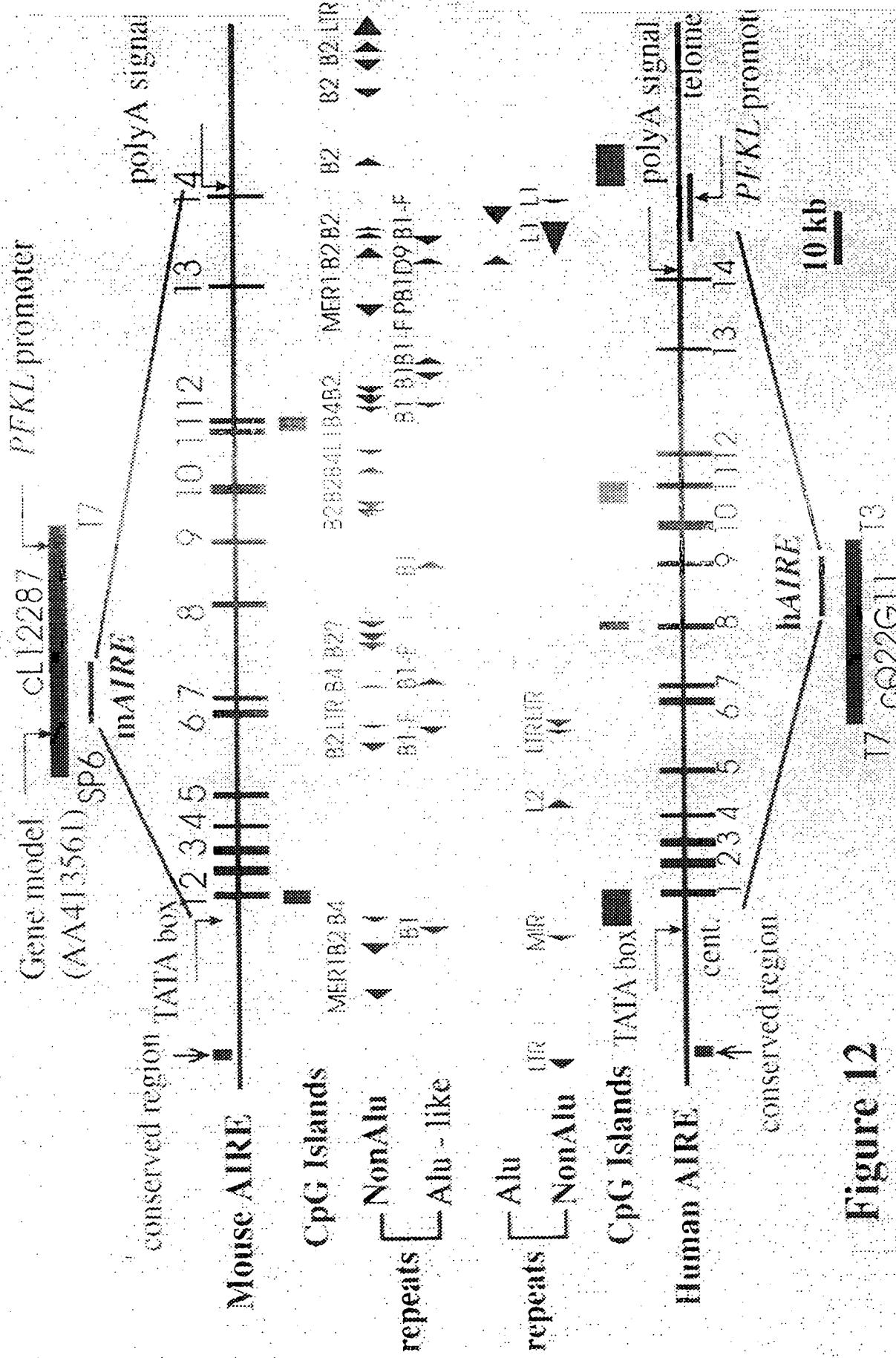


Figure 12

## HSAJ9610 (horizontal) vs. AF073797 (vertical)

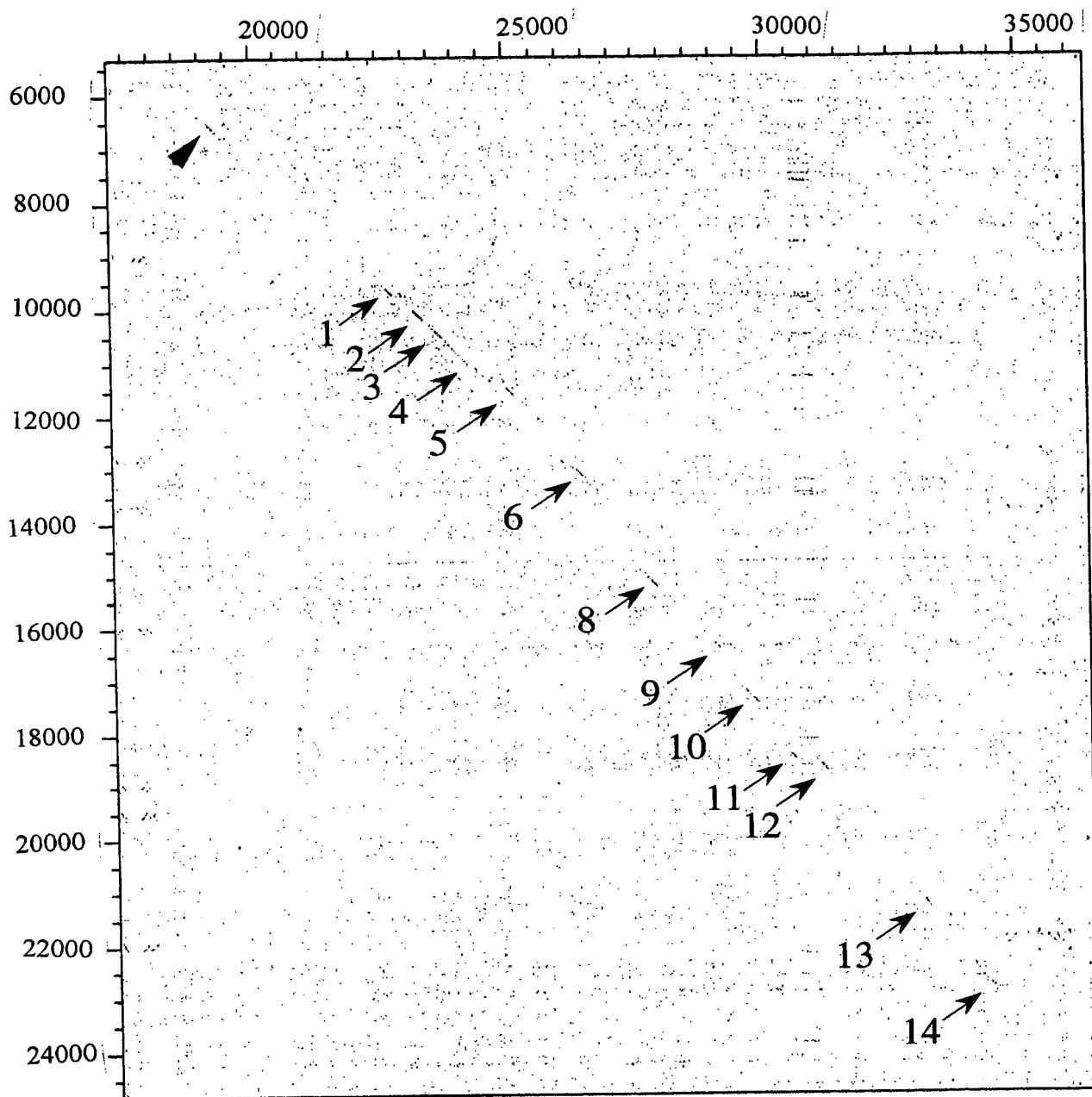


Figure 13A

6486 GTCGCACTG TCACGGAAAC CCCAACCTGT GATGGAAAGT CCGAAATTCT ACAGGGAGCTT TTCTGTTGAT CTCAGTCAG AGGCTGGGG  
LIRE AGGGGGCTGG TGTGGAAAGC CCCAACGGAT GGTGGAAAGT CGGAAATTCT ACAGGGGGCTT CTTGTTAAA CCTCCATGCA AGGGCTGGG  
19186 19275  
lons.

Figure 13B

19/27

	10	30	50	
1	ATGGCAGGTGGGATGGAATGCTACGCCGCTGCTGAGGCTGCACCGCACCGAGATCGCG			60
1	M A G G D G M L R R R L L R L H R T E I A	70	90	110
61	GTGCCATAGACAGTGCCTTCCGCTGCTGCATGCTCTAGCCGACCACGACGTGGTCCCT			120
21	V A I D S A F P L L H A L A D H D V V P	130	150	170
121	GAGGACAAGTTCCAGGAGACGCTCCGTCTGAAGGAGAAGGAAGGCTGCCCGCAGGCCCTTC			180
41	E D K F Q E T L R L K E K E G C P Q A F	190	210	230
181	CACGCCCTGCTGTCCTGGCTCCTGACCCGGGACAGTGGGGCCATCCTGGATTCTGGAGG			240
61	H A L L S W L L T R D S G A I L D F W R	250	270	290
241	ATTCTCTTAAGGACTACAATCTGGAGCGGTACAGCCGCCTGCATAGCATCCTGGACGGC			300
81	I L F K D Y N L E R Y S R L H S I L D G	310	330	350
301	TTCCCCAAAGATGTGGACCTAAACCAAGTCCCGGAAAGGGAGAAAGCCCCTTGCTGGTCCC			360
101	F P K D V D L N Q S R K G R K P L A G P	370	390	410
361	AAGGCCGCGGTACTGCCACCCAGACCCCCCACCAAGAGAAAAGCACTGGAGGAGCCTCGA			420
121	K A A V L P P R P P T K R K A L E E P R	430	450	470
421	GCCACCCCCACCAGCAACTCTGGCCTCAAAGAGCGTCTCCAGCCCAGGCTCCACCTGAAG			480
141	A T P P A T L A S K S V S S P G S H L K	490	510	530
481	ACTAAGCCCCCTAAGAAGCCAGATGGCAACTTGGAGTCACAGCACCTCCTTGGAAAC			540
161	T K P P K K P D G N L E S Q H L P L G N	550	570	590
541	GGAATTCAAGACCATGGCAGCTCTGTCCAGAGAGCTGTGACCGTGGCCTCTGGGATGTT			600
181	G I Q T M A A S V Q R A V T V A S G D V	610	630	650
601	CCAGGAACCCGAGGGGCCGTGGAAGGGATCCTTATCCAGCAGGTGTTGAGTCAGGAAGA			660
201	P G T R G A V E G I L I Q Q V F E S G R	670	690	710
661	TCCAAGAAGTGCATTCAAGTGGGGAGAGTTTATACACCCAACAAAGTCGAAGACCCC			720
221	S K K C I Q V G G E F Y T P N K F E D P			240

Figure 14A

20/27

	730	750	770	
721	AGTGGCAATTGAAGAACAGGCCGGAGTGGTAGCAGCCTAAAGCCAGTGGTCCGAGCC			780
241	S G N L K N K A R S G S S L K P V V R A			260
	790	810	830	
781	AAGGGAGCCCAGGTCACTATACCTGGTAGAGATGAGCAGAAAGTGGCCAGCAGTGTGGG			840
261	K G A Q V T I P G R D E Q K V G Q Q C G			280
	850	870	890	
841	GTTCCCTCCCCTTCATCCCTCCCCAGTGGAGCCAGGTTAACAGAAGAACGAGGATGAG			900
281	V P P L P S L P S E P Q V N Q K N E D E			300
	910	930	950	
901	TGTGCCGTGTGCCACGACGGAGGTGAGCTCATCTGTTGTACGGCTGTCCCCGGGCCTTC			960
301	C A V C H D G G E L I C C C D G C P R A F			320
	970	990	1010	
961	CACCTGGCTTGCCTGTCCCCACCTCTGCAGGAGATCCCCAGTGGCCTCTGGAGATGCTCC			1020
321	H L A C L S P P L Q E I P S G L W R C S			340
	1030	1050	1070	
1021	TGCTGCCTCCAGGGCAGAGTCCAACAGAACCTGTCCCAGCCTGAGGTGTCCAGGCCCCG			1080
341	C C L Q G R V Q Q N L S Q P E V S R P P			360
	1090	1110	1130	
1081	GAGCTACCTGCAGAGACCCGATCCTCGTGGACTGAGGTAGCTTCAGAGAAAACCAGG			1140
361	E L P A E T P I L V G L R S A S E K T R			380
	1150	1170	1190	
1141	GGCCCATCCAGGGAGCTCAAAGCCAGCTGTGATGCTGTCACATATGTGAACCTGCTG			1200
381	G P S R E L K A S S D A A V T Y V N L L			400
	1210	1230	1250	
1201	GCCCCGCACCCCTGCAGCTCCTCTGCTGGAGCCTTCAGCACTGTGCCCTACTGAGTGCT			1260
401	A P H P A A P L L E P S A L C P L L S A			420
	1270	1290	1310	
1261	GGGAATGAGGGGGGCCAGGTCCAGCACCAAGCGCGCGATGCAGTGTGTGGCGATGGC			1320
421	G N E G R P G P A P S A R C S V C G D G			440
	1330	1350	1370	
1321	ACCGAGGTGTTGCGGTGTGCACACTGTGCCGTGCCCTCCACTGGCGCTGCCACTTCCCG			1380
441	T E V L R C A H C A A A F H W R C H F P			460
	1390	1410	1430	
1381	ACGGCCGCCGCCGGCCGGGACCAATCTCGCTGCAAATCCTGCTCTGCAGACTCGACT			1440
461	T A A A R P G T N L R C K S C S A D S T			480
	1450	1470	1490	

Figure 14B

21/27

1441	CCCACGCCAGGCACACCGGGCGAAGCTGTACCCACCTCTGGGCCCGTCCAGCACCTGGG	1500
481	P T P G T P G E A V P T S G P R P A P G 1510 1530 1550	500
1501	CTTGCCAAGgttagGGGACGACTCTGCTAGTCACGACCCCTGTTCTACATAGGGACGACCTG	1560
501	L A K V G D D S A S H D P V L H R D D L 1570 1590 1610	520
1561	GAGTCCCTCCTCAATGAGCACTCATTGACGGCATCCTGCAGTGGGCCATCCAGAGCATG	1620
521	E S L L N E H S F D G I L Q W A I Q S M 1630 1650	540
1621	TCACGCCCGCTGGCCGAGACACCACCCCTTCTCTTCC	1656
541	S R P L A E T P P F S S	552

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Figure 14C

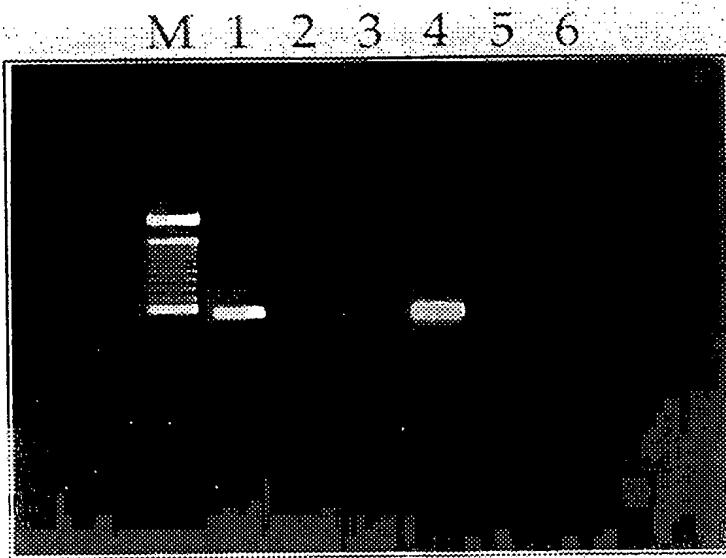


Figure 15

23/27

Human AIRE	~MATDA <u>PLRR</u> <u>LL</u> RLHRTEIA VAVDSAFPLL HALADHDVVP EDKFQETLHL
Mouse AIRE	MAGGDGMLRR <u>LL</u> RLHRTEIA VAIDSAFPLL HALADHDVVP EDKFQETLRL
Consensus	---D--- <u>LRR</u> <u>LL</u> RLHRTEIA VA-DSAFPLL HALADHDVVP EDKFQETL-L
51	
Human AIRE	KEKEGCPQAF HALLSWLLTQ DSTAILDFWR VLFKDYNLER YGRLQPILDS
Mouse AIRE	KEKEGCPQAF HALLSWLLTR DSGAILDFWR ILFKDYNLER YSRLHSILDG
Consensus	KEKEGCPQAF HALLSWLLT- DS-AIILDFWR -LFKDYNLER Y-RL--ILD-
101	
Human AIRE	FPKDVDLSQP RKGRKPPAVP KALVPPRRLP TKRKASEEAR AAAPAALT
Mouse AIRE	FPKDVDLNQS RKGRKPLAGP KAAVLPPIPP TKRKALEEPR ATPPATLASK
Consensus	FPKDVDL-Q- <u>RKGRKP</u> -A-P KA-V-PPR-P <u>TKRKA</u> -EE-R A--PA-L---
151	
Human AIRE	GTASPGSQLK AKPPKKPESS AEQQRLPLGN GIQTMSASVQ RAVAMSSGDV
Mouse AIRE	SVSSPGSHLK TKPPKKPDGN LESQHPLGN GIQTMAASVQ RAVTVASGDV
Consensus	---SPGS-LK -KPPKKP--- -E-Q-LPLGN GIQTM-ASVQ RAV---SGDV
201	
Human AIRE	PGARGAVEGI LIQQVFESGG SKKCIQVGGE FYTPSKFED. SGSGKKNKARS
Mouse AIRE	PGTRGAVEGI LIQQVFESGR SKKCIQVGGE FYTPNKFEDP SGNLKNKARS
Consensus	<u>PG-RGAVEGI</u> <u>LIQQVFESG-</u> <u>SKKCIQVGGE</u> <u>FYTP-KFED-</u> SG--KNKARS
251	
Human AIRE	SSGPKPLVRA KGAQGAAPGG GEARLGQQGS VPAPLALPSD PQLHQKNEDE
Mouse AIRE	GSSLKPVVRA KGAQVTIPGR DEQKVGQQCG VPPPLPSLPSE PQVNQKNEDE
Consensus	-S-- <u>KP-VRA</u> <u>KGAQ</u> --- <u>PG</u> -E--- <u>GQQ</u> -- VP---LPS- PQ--QKNEDE
301	
Human AIRE	CAVCRDGEL ICCDGCPRAF HLACLSPPLR EIPSGTWRCs SCLQATVQEV
Mouse AIRE	CAVCHDGEL ICCDGCPRAF HLACLSPPLQ EIPSGLWRCS CCLQGRVQZN
Consensus	CAVC-DGGEL ICCDGCPRAF HLACLSPPL- EIPSG-WRCs -CLQ--VQ--
351	
Human AIRE	QPRAEPRPQ EPPVETPLPP GLRSAGEEVr GPPGEPLAGM DTTLVYKHLp
Mouse AIRE	LSQPEVSRPP ELPATEPILV GLRSASEKTR GPSRELKASS DAAVTVVNLL
Consensus	----E--RP- E-P-ETP--- GLRSA-E--R GP--E--A-- D----Y--L-
401	
Human AIRE	APPSAAPLPG LDSSALHPLL CVGPEGQQNL APGARCGVCG DGTDVLRCTH
Mouse AIRE	APHPAAPL.. LEPSALCPPL SAGNEGRPGP APSARCSVCG DGTEVLRCAH
Consensus	AP--AAPL-- L--SAL-PLL --G-EG---- AP-ARC-VCG DGT-VLRC-H
451	
Human AIRE	CAAFFHWRCH FPAGTSRPGT GLRCRSCSGD VTPAP.VEGV LAP. SPARLA
Mouse AIRE	CAAFFHWRCH FPTAAARP GT NLRCKSCSAD STPTPGTPGE AVPTSGPRPA
Consensus	CAAFFHWRCH F----RPGT -LRC-SCS-D -TP-P---G- --P-S--R-A
501	
Human AIRE	PGPAK..DDT ASHEPALHRD DLESLLSEHT FDGILQWAIQ SMARPAAPP?
Mouse AIRE	PGLAKVGDDS ASHDPVLHRD DLESLLNEHS FDGILQWAIQ SMSRPLAET?
Consensus	PG-AK--DD- ASH-?-LHRD DLESLL-EH- FDGILQWAIQ SM-RP-A--?
551	
Human AIRE	S---
Mouse AIRE	PFSS
Consensus	----

Figure 16

00000000000000000000000000000000

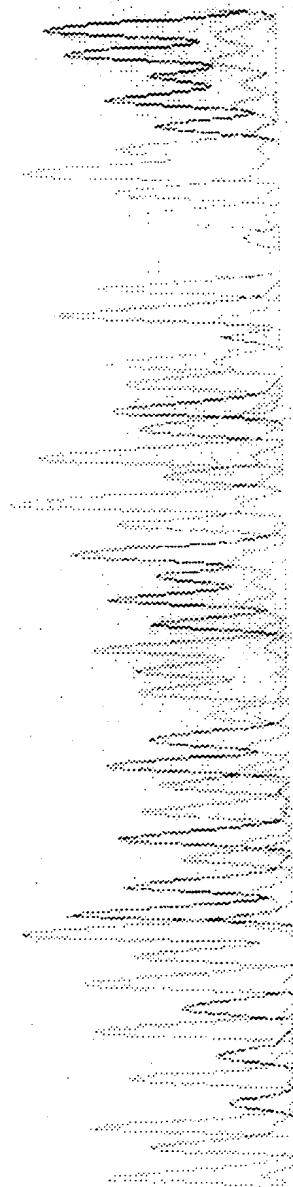
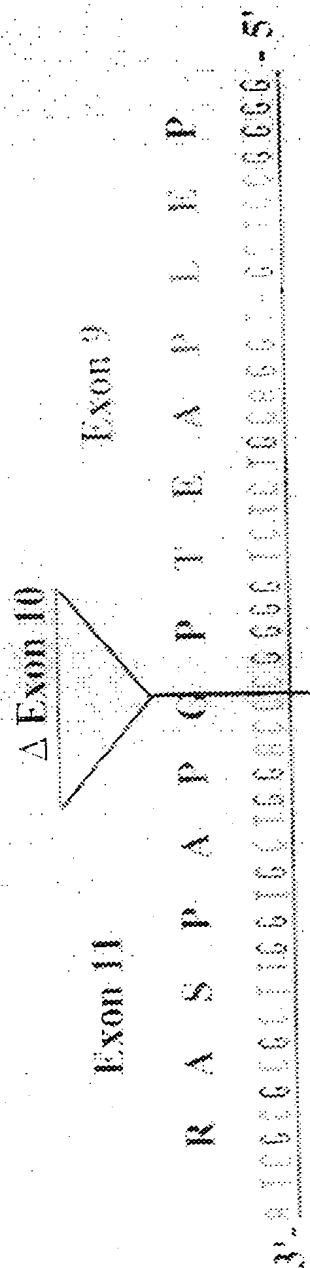


FIGURE 17 A

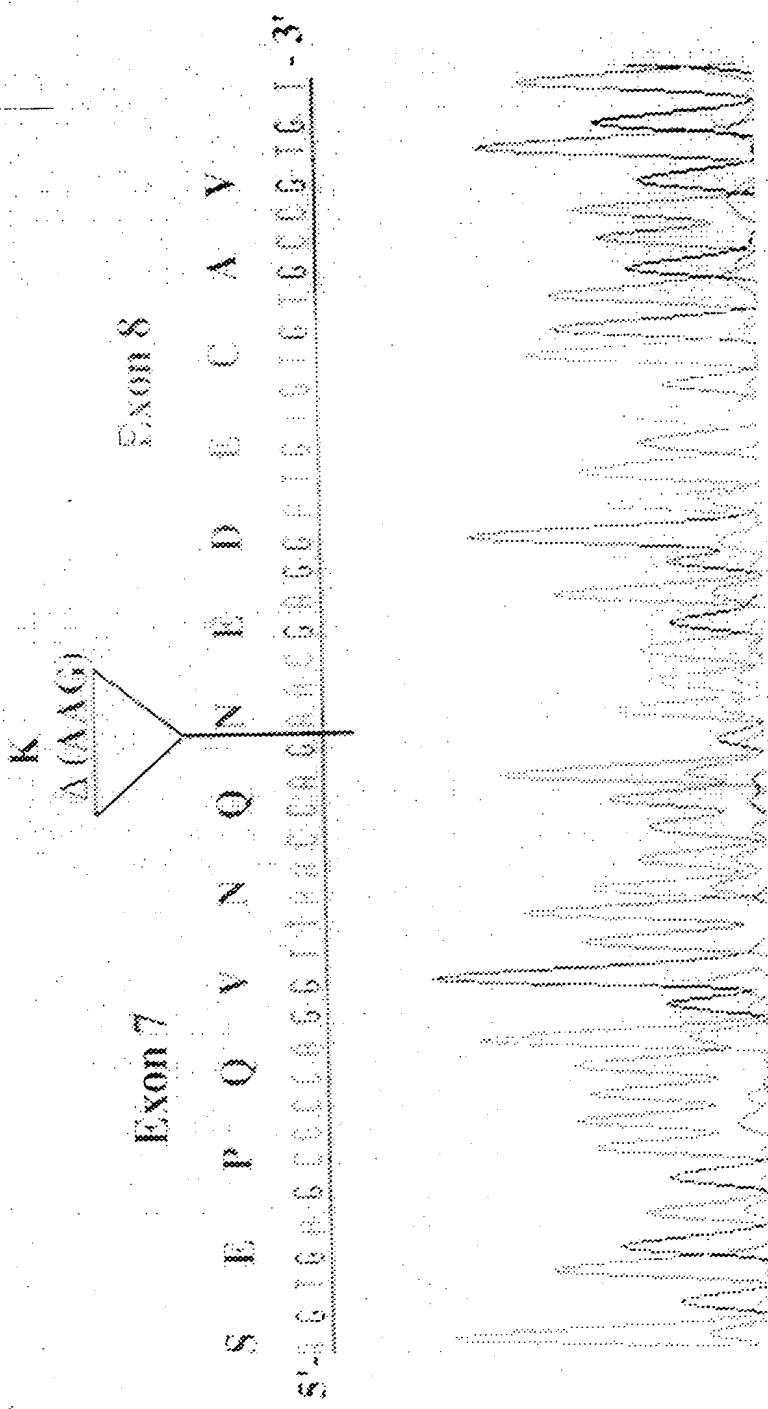


FIGURE 17B

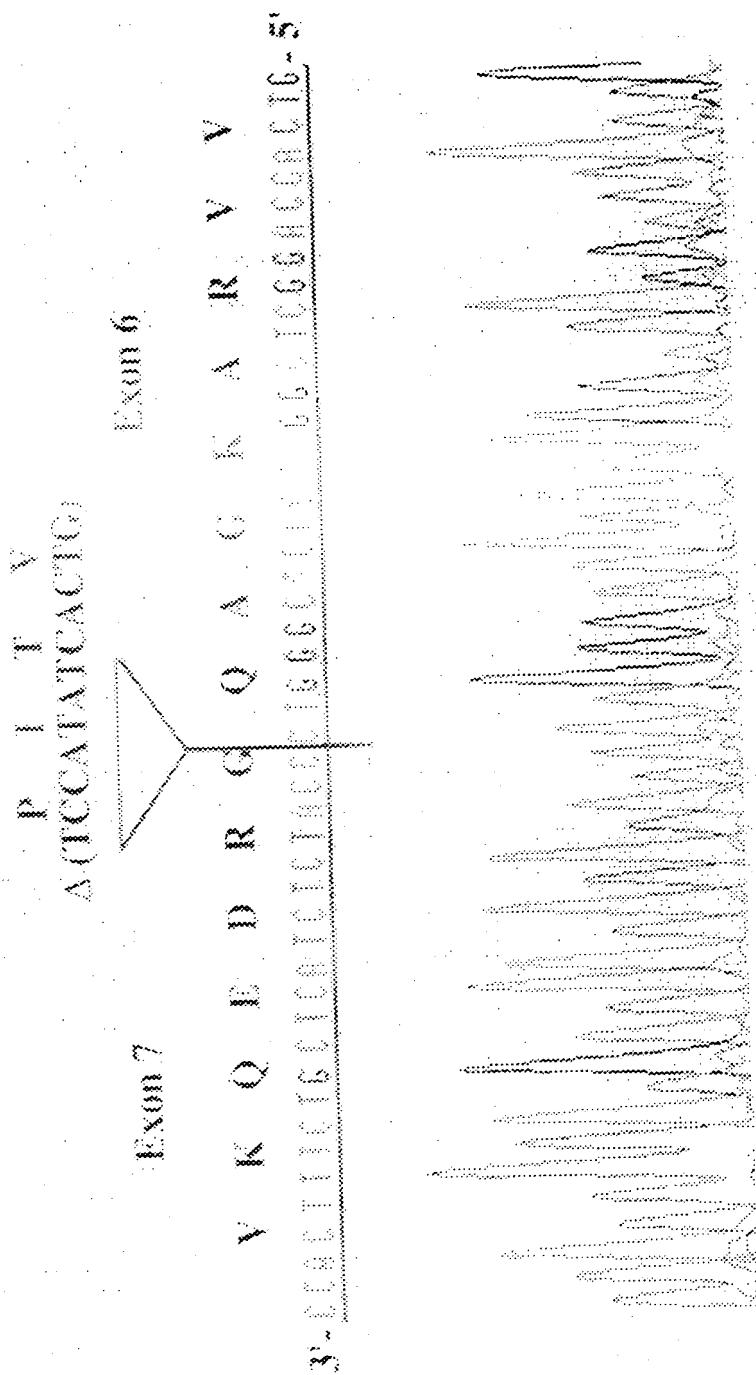


FIGURE 17C

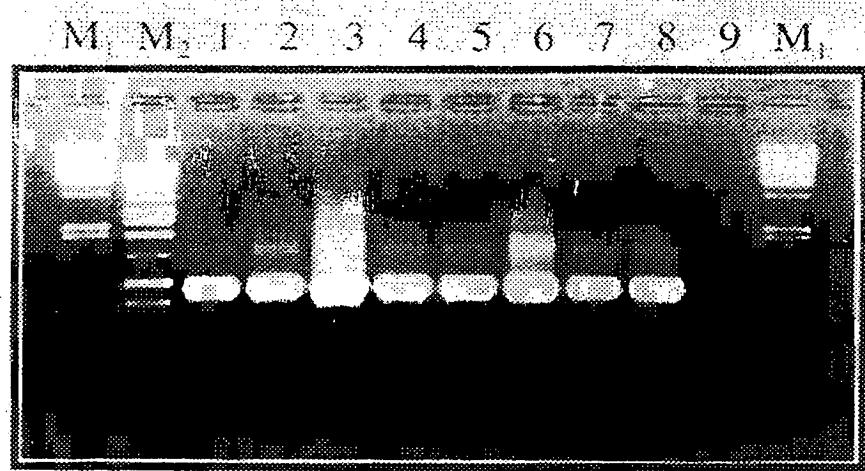


Figure 18